

**Exhibit C**

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ\_180 252 aa

Sequence 2: G\_kaustophilus\_deltaprime 328 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060911-20060223.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score: 5465

Alignment Score 1571

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060911-20060223.aln]

SEQ_180	MRWEQLAKRQPVVAKMLQSGLEKGRISHAYLFEGQRGTGKKAASLLLAKR	50
G_kaustophilus_deltaprime	MRWEQLAKRQPVVAKMLQSGLEKGRISHAYLFEGQRGTGKKAASLLLAKR	50
	*****	

SEQ_180	LFCLSPIGVSPCLECRNCRRIDSGNHPDVRVIGPDGGSIKKEQIEWLQQE	100
G_kaustophilus_deltaprime	LFCLSPIGVSPCLECRNCRRIDSGNHPDVRVISPDGGSIKKEQIEWLQQE	100
	*****	

SEQ_180	FSKTAVESDKKMYIVEADQMTTSAANSLLKFLEEPHPGTAVAVLLTEQYH	150
G_kaustophilus_deltaprime	FSKTAVESDKKMYIVEADQMTTSAANSLLKFLEEPHPGTAVAVLLTEQYH	150
	*****	

SEQ_180	RLLGTIVSRCQVLSFRPLPPAELAQGLVEEHVPLPLALLAAHLTNSFEEA	200
G_kaustophilus_deltaprime	RLLGTIVSRCQVLSFRPLPPAELAQGLVEEHVPLPLALLAAHLTNSFEEA	200
	*****	

SEQ_180	LALAKDSWFAEARTLVLQWYEMLGKPELQLLFFIHDRLFPHFLESHQLDL	250
G_kaustophilus_deltaprime	LALAKDSWFAEARTLVLQWYEMLGKPELQLLFFIHDRLFPHFLESHQLDL	250
	*****	

SEQ_180	GL-----	252
G_kaustophilus_deltaprime	GLDLLLLYRDLLHIQAGQMDGVLYRDQLDRLQRWALACPQRRILAGMEA	300
	**	

SEQ_180	-----	
G_kaustophilus_deltaprime	ILQAKTRLNTTNMSTALLVEQLVQLKR	328